

1 / 3 6

SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

THE UNIVERSITY OF TOKYO

<120> METHODS OF DETECTING METHYL TRANSFERASE ACTIVITY AND METHODS OF
SCREENING FOR METHYL TRANSFERASE ACTIVITY MODULATORS

<130> ONC-A0310P

<150> US 60/538, 658

<151> 2004-01-23

<160> 55

<170> PatentIn version 3.3

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2 / 3 6

acaacagcct caagatcatc ag

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3 / 3 6

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4 / 3 6

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5 / 3 6

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6 / 3 6

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7 / 3 6

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caaacaggaa ccaagaacaa gtc

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8 / 3 6

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9 / 36

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1 2 / 3 6

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ggcaccacctt tcgtgcagta ccagg

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1 4 / 3 6

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gaccaaagcc caggcagtga gagtg

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1 5 / 3 6

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aggggtgggt ttatttagcac ccagg

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binding assay

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1 7 / 3 6

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ccctttgatc ttacc

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1 8 / 3 6

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ggtaagatca aaggg

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binding assay

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ccctttggcc ttacc

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binding assay

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ggtaaggcca aaggg

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cggaaattctg gcgtcgtctg cgaccgcgt

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20 / 36

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32

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22 / 36

<212> DNA

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gggttacatt accggcgctc ctcactggtc

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<213> Artificial

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agcgggcctg gtaccaaatt tgtg

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<210> 47

<211> 24

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<213> Artificial

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<223> An artificially synthesized primer sequence to amplify the fragment of Nkx2.8 promoter by PCR

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ccgggatgct agcgcatatca cagc

24

<210> 48

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24 / 36

<212> DNA

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<223> An artificially synthesized oligonucleotide sequence for plasmids
expressing siRNA to ZNFN3A1

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expressing siRNA to ZNFN3A1

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25 / 36

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Met Glu Pro Leu Lys Val

1 5

gaa aag ttc gca acc gcc aac agg gga aac ggg ctg cgc gcc gtg acc 161

Glu Lys Phe Ala Thr Ala Asn Arg Gly Asn Gly Leu Arg Ala Val Thr

10 15 20

ccg ctg cgc ccc gga gag cta ctc ttc cgc tcg gat ccc ttg gcg tac 209

Pro Leu Arg Pro Gly Glu Leu Leu Phe Arg Ser Asp Pro Leu Ala Tyr

25 30 35

acg gtg tgc aag ggg agt cgt ggc gtc gtc tgc gac cgc tgc ctt ctc 257

Thr Val Cys Lys Gly Ser Arg Gly Val Val Cys Asp Arg Cys Leu Leu

40 45 50

26 / 36

ggg aag gaa aag ctg atg cga tgc tct cag tgc cgc gtc gcc aaa tac	305		
Gly Lys Glu Lys Leu Met Arg Cys Ser Gln Cys Arg Val Ala Lys Tyr			
55	60	65	70
tgt agt gct aag tgt cag aaa aaa gct tgg cca gac cac aag cgg gaa	353		
Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp Pro Asp His Lys Arg Glu			
75	80	85	
tgc aaa tgc ctt aaa agc tgc aaa ccc aga tat cct cca gac tcc gtt	401		
Cys Lys Cys Leu Lys Ser Cys Lys Pro Arg Tyr Pro Pro Asp Ser Val			
90	95	100	
cga ctt ctt ggc aga gtt gtc ttc aaa ctt atg gat gga gca cct tca	449		
Arg Leu Leu Gly Arg Val Val Phe Lys Leu Met Asp Gly Ala Pro Ser			
105	110	115	
gaa tca gag aag ctt tac tca ttt tat gat ctg gag tca aat att aac	497		
Glu Ser Glu Lys Leu Tyr Ser Phe Tyr Asp Leu Glu Ser Asn Ile Asn			
120	125	130	
aaa ctg act gaa gat aag aaa gag ggc ctc agg caa ctc gta atg aca	545		
Lys Leu Thr Glu Asp Lys Lys Glu Gly Leu Arg Gln Leu Val Met Thr			
135	140	145	150
ttt caa cat ttc atg aga gaa gaa ata cag gat gcc tct cag ctg cca	593		

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Phe Gln His Phe Met Arg Glu Glu Ile Gln Asp Ala Ser Gln Leu Pro
155 160 165

cct gcc ttt gac ctt ttt gaa gcc ttt gca aaa gtg atc tgc aac tct 641
Pro Ala Phe Asp Leu Phe Glu Ala Phe Ala Lys Val Ile Cys Asn Ser
170 175 180

ttc acc atc tgt aat gcg gag atg cag gaa gtt ggt gtt ggc cta tat 689
Phe Thr Ile Cys Asn Ala Glu Met Gln Glu Val Gly Val Gly Leu Tyr
185 190 195

ccc agt atc tct ttg ctc aat cac agc tgt gac ccc aac tgt tcg att 737
Pro Ser Ile Ser Leu Leu Asn His Ser Cys Asp Pro Asn Cys Ser Ile
200 205 210

gtg ttc aat ggg ccc cac ctc tta ctg cga gca gtc cga gac atc gag 785
Val Phe Asn Gly Pro His Leu Leu Leu Arg Ala Val Arg Asp Ile Glu
215 220 225 230

gtg gga gag gag ctc acc atc tgc tac ctg gat atg ctg atg acc agt 833
Val Gly Glu Glu Leu Thr Ile Cys Tyr Leu Asp Met Leu Met Thr Ser
235 240 245

gag gag cgc cg^g aag cag ctg agg gac cag tac tgc ttt gaa tgt gac 881
Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln Tyr Cys Phe Glu Cys Asp
250 255 260

28 / 36

tgt ttc cgt tgc caa acc cag gac aag gat gct gat atg cta act ggt 929
Cys Phe Arg Cys Gln Thr Gln Asp Lys Asp Ala Asp Met Leu Thr Gly
265 270 275

gat gag caa gta tgg aag gaa gtt caa gaa tcc ctg aaa aaa att gaa 977
Asp Glu Gln Val Trp Lys Glu Val Gln Glu Ser Leu Lys Lys Ile Glu
280 285 290

gaa ctg aag gca cac tgg aag tgg gag cag gtt ctg gcc atg tgc cag 1025
Glu Leu Lys Ala His Trp Lys Trp Glu Gln Val Leu Ala Met Cys Gln
295 300 305 310

gcg atc ata agc agc aat tct gaa cgg ctt ccc gat atc aac atc tac 1073
Ala Ile Ile Ser Ser Asn Ser Glu Arg Leu Pro Asp Ile Asn Ile Tyr
315 320 325

cag ctg aag gtg ctc gac tgc gcc atg gat gcc tgc atc aac ctc ggc 1121
Gln Leu Lys Val Leu Asp Cys Ala Met Asp Ala Cys Ile Asn Leu Gly
330 335 340

ctg ttg gag gaa gcc ttg ttc tat ggt act cgg acc atg gag cca tac 1169
Leu Leu Glu Glu Ala Leu Phe Tyr Gly Thr Arg Thr Met Glu Pro Tyr
345 350 355

agg att ttt ttc cca gga agc cat ccc gtc aga ggg gtt caa gtg atg 1217

29 / 36

Arg Ile Phe Phe Pro Gly Ser His Pro Val Arg Gly Val Gln Val Met

360 365 370

aaa gtt ggc aaa ctg cag cta cat caa ggc atg ttt ccc caa gca atg 1265

Lys Val Gly Lys Leu Gln Leu His Gln Gly Met Phe Pro Gln Ala Met

375 380 385 390

aag aat ctg aga ctg gct ttt gat att atg aga gtg aca cat ggc aga 1313

Lys Asn Leu Arg Leu Ala Phe Asp Ile Met Arg Val Thr His Gly Arg

395 400 405

gaa cac agc ctg att gaa gat ttg att cta ctt tta gaa gaa tgc gac 1361

Glu His Ser Leu Ile Glu Asp Leu Ile Leu Leu Glu Glu Cys Asp

410 415 420

gcc aac atc aga gca tcc taa ggaaacgcag tcagagggaa atacggcgtg 1412

Ala Asn Ile Arg Ala Ser

425

tgtctttgtt gaatgccta ttgaggcac acactctatg ctttgttagc tgtgtgaacc 1472

tctcttattg gaaattctgt tccgttttg tgtaggtaaa taaaggcaga catggttgc 1532

aaaccacaag aatcattagt tgtagagaag cacgattata ataaattcaa aacatttggt 1592

tgaggatgcc aaaaaaaaaaaaaaaa 1622

30 / 36

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<213> Homo sapiens

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Met Glu Pro Leu Lys Val Glu Lys Phe Ala Thr Ala Asn Arg Gly Asn

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Gly Leu Arg Ala Val Thr Pro Leu Arg Pro Gly Glu Leu Leu Phe Arg

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Ser Asp Pro Leu Ala Tyr Thr Val Cys Lys Gly Ser Arg Gly Val Val

35 40 45

Cys Asp Arg Cys Leu Leu Gly Lys Glu Lys Leu Met Arg Cys Ser Gln

50 55 60

Cys Arg Val Ala Lys Tyr Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp

31 / 36

65

70

75

80

Pro Asp His Lys Arg Glu Cys Lys Cys Leu Lys Ser Cys Lys Pro Arg

85

90

95

Tyr Pro Pro Asp Ser Val Arg Leu Leu Gly Arg Val Val Phe Lys Leu

100

105

110

Met Asp Gly Ala Pro Ser Glu Ser Glu Lys Leu Tyr Ser Phe Tyr Asp

115

120

125

Leu Glu Ser Asn Ile Asn Lys Leu Thr Glu Asp Lys Lys Glu Gly Leu

130

135

140

Arg Gln Leu Val Met Thr Phe Gln His Phe Met Arg Glu Glu Ile Gln

145

150

155

160

Asp Ala Ser Gln Leu Pro Pro Ala Phe Asp Leu Phe Glu Ala Phe Ala

165

170

175

3 2 / 3 6

Lys Val Ile Cys Asn Ser Phe Thr Ile Cys Asn Ala Glu Met Gln Glu

180 185 190

Val Gly Val Gly Leu Tyr Pro Ser Ile Ser Leu Leu Asn His Ser Cys

195 200 205

Asp Pro Asn Cys Ser Ile Val Phe Asn Gly Pro His Leu Leu Leu Arg

210 215 220

Ala Val Arg Asp Ile Glu Val Gly Glu Glu Leu Thr Ile Cys Tyr Leu

225 230 235 240

Asp Met Leu Met Thr Ser Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln

245 250 255

Tyr Cys Phe Glu Cys Asp Cys Phe Arg Cys Gln Thr Gln Asp Lys Asp

260 265 270

Ala Asp Met Leu Thr Gly Asp Glu Gln Val Trp Lys Glu Val Gln Glu

33 / 36

275 280 285

Ser Leu Lys Lys Ile Glu Glu Leu Lys Ala His Trp Lys Trp Glu Gln

290 295 300

Val Leu Ala Met Cys Gln Ala Ile Ile Ser Ser Asn Ser Glu Arg Leu

305 310 315 320

Pro Asp Ile Asn Ile Tyr Gln Leu Lys Val Leu Asp Cys Ala Met Asp

325 330 335

Ala Cys Ile Asn Leu Gly Leu Leu Glu Glu Ala Leu Phe Tyr Gly Thr

340 345 350

Arg Thr Met Glu Pro Tyr Arg Ile Phe Phe Pro Gly Ser His Pro Val

355 360 365

Arg Gly Val Gln Val Met Lys Val Gly Lys Leu Gln Leu His Gln Gly

370 375 380

3 4 / 3 6

Met Phe Pro Gln Ala Met Lys Asn Leu Arg Leu Ala Phe Asp Ile Met

385 390 395 400

Arg Val Thr His Gly Arg Glu His Ser Leu Ile Glu Asp Leu Ile Leu

405 410 415

Leu Leu Glu Glu Cys Asp Ala Asn Ile Arg Ala Ser

420 425

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<212> PRT

<213> Homo sapiens

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Asn His Ser Cys Asp Pro Asn

1 5

<210> 53

<211> 8

3 5 / 3 6

<212> PRT

<213> Homo sapiens

<400> 53

Gly Glu Glu Leu Thr Ile Cys Tyr

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<223> "Xaa" indicates any amino acid

<400> 54

Asn His Ser Cys Xaa Xaa Asn

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3 6 / 3 6

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<222> (5)..(7)

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Gly Glu Glu Leu Xaa Xaa Xaa Tyr

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5